

E HU SONG/AU 25
L1 56 S (E3)
E ZHONG MIN/AU 25
L2 116 S (E3)
L3 1 S L2 AND SERINE
L4 1 S L3 AND ANTIBOD?
E LADUNGA ISTVAN/AU 25
L5 21 S (E3)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 15:27:28 ON 01 NOV 2006

L6 16410 S SERINE (S) PROTEASE (S) INHIBITOR?
L7 248 S L6 (S) ANTIBOD?
L8 102 DUP REM L7 (146 DUPLICATES REMOVED)
L9 102 SORT L8 PY A



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- If making selections (e.g., Subheadings, etc.), use the [Send to Search Box](#) feature to see PubMed records with those specifications.
- Select PubMed under the Links menu to retrieve all records for the MeSH Term.
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1: Serpins

Links

A family of serine proteinase inhibitors which are similar in amino acid sequence and mechanism of inhibition, but differ in their specificity toward proteolytic enzymes. This family includes alpha 1-antitrypsin, angiotensinogen, ovalbumin, antiplasmin, alpha 1-antichymotrypsin, thyroxine-binding protein, complement 1 inactivators, antithrombin III, heparin cofactor II, plasminogen inactivators, gene Y protein, placental plasminogen activator inhibitor, and barley Z protein. Some members of the serpin family may be substrates rather than inhibitors of SERINE ENDOPEPTIDASES, and some serpins occur in plants where their function is not known.

Year introduced: 1990

Subheadings: This list includes those paired at least once with this heading in MEDLINE and may not reflect current rules for allowable combinations.

☐ administration and dosage ☐ adverse effects ☐ analysis ☐ biosynthesis ☐ blood
☐ cerebrospinal fluid ☐ chemical synthesis ☐ chemistry ☐ classification
☐ deficiency ☐ diagnostic use ☐ drug effects ☐ genetics ☐ history ☐ immunology
☐ isolation and purification ☐ metabolism ☐ pharmacokinetics ☐ pharmacology
☐ physiology ☐ radiation effects ☐ secretion ☐ therapeutic use ☐ toxicity
☐ ultrastructure ☐ urine

☐ Restrict Search to Major Topic headings only

☐ Do Not Explode this term (i.e., do not include MeSH terms found below this term in the MeSH tree).

Entry Terms:

- Serpin Superfamily
- Superfamily, Serpin

Previous Indexing:

- [Enzyme Inhibitors \(1968-1978\)](#)

- [Protease Inhibitors \(1979-1989\)](#)

Pharmacologic Action:

- Serine Proteinase Inhibitors

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Serpins

[alpha 1-Antichymotrypsin](#)

[alpha 1-Antitrypsin](#)

[Angiotensinogen](#)

[Antiplasmin](#)

[Antithrombins](#)

[Antithrombin III](#)

[Heparin Cofactor II](#)

[Hirudins](#)

[Complement C1 Inactivator Proteins](#)

[HSP47 Heat-Shock Proteins](#)

[Ovalbumin](#)

[Plasminogen Inactivators](#)

[Plasminogen Activator Inhibitor 1](#)

[Plasminogen Activator Inhibitor 2](#)

[Protein C Inhibitor](#)

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GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: October 21, 2006, 01:15:26 ; Search time 615 Seconds
(without alignments)
610.782 Million cell updates/sec

Title: US-09-903-582-2
Perfect score: 1315
Sequence: 1 MKPGGFWLHLTLLGASLPAA.....YNSDSSLTLREFYMAFRQKC 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1315	100.0	246	1	PCT-US02-21670-2	Sequence 2, Appli
2	1315	100.0	246	1	PCT-US04-37982-3430	Sequence 3430, Ap
3	1315	100.0	246	29	US-09-903-582-2	Sequence 2, Appli
4	1315	100.0	246	41	US-11-124-368A-170	Sequence 170, App
5	1292	98.3	243	1	PCT-US02-21670-4	Sequence 4, Appli
6	1292	98.3	243	29	US-09-903-582-4	Sequence 4, Appli
7	1292	98.3	491	41	US-11-166-372-2150	Sequence 2150, Ap
8	1292	98.3	491	41	US-11-166-372A-2150	Sequence 2150, Ap
9	1292	98.3	838	1	PCT-US04-37982-3432	Sequence 3432, Ap
10	1292	98.3	842	24	US-09-432-359-2	Sequence 2, Appli
11	1292	98.3	842	25	US-09-544-511-16	Sequence 16, Appl
12	1292	98.3	842	27	US-09-703-211-2	Sequence 2, Appli
13	1292	98.3	842	27	US-09-703-211A-2	Sequence 2, Appli
14	1292	98.3	842	29	US-09-965-212-16	Sequence 16, Appl
15	1292	98.3	842	29	US-09-966-545-16	Sequence 16, Appl
16	1292	98.3	842	29	US-09-966-546-16	Sequence 16, Appl
17	1292	98.3	842	31	US-10-189-940-16	Sequence 16, Appl
18	1292	98.3	842	31	US-10-189-940-87	Sequence 87, Appl
19	1292	98.3	842	34	US-10-428-275-240	Sequence 240, App
20	1292	98.3	842	34	US-10-428-275-252	Sequence 252, App
21	1292	98.3	842	34	US-10-428-275-270	Sequence 270, App
22	1292	98.3	842	34	US-10-428-275-278	Sequence 278, App
23	1292	98.3	842	39	US-10-971-479-16	Sequence 16, Appl
24	1292	98.3	842	39	US-10-971-479-87	Sequence 87, Appl
25	1292	98.3	842	41	US-11-124-368A-171	Sequence 171, App
26	1292	98.3	846	31	US-10-189-940-88	Sequence 88, Appl
27	1292	98.3	846	31	US-10-189-940-148	Sequence 148, App
28	1292	98.3	846	34	US-10-428-275-242	Sequence 242, App
29	1292	98.3	846	34	US-10-428-275-250	Sequence 250, App
30	1292	98.3	846	39	US-10-971-479-88	Sequence 88, Appl
31	1292	98.3	846	39	US-10-971-479-148	Sequence 148, App

32	1292	98.3	849	34	US-10-428-275-254
33	1288	97.9	837	31	US-10-189-940-126
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35	1288	97.9	837	39	US-10-971-479-126
36	1287	97.9	842	34	US-10-428-275-276
37	1284	97.6	842	34	US-10-428-275-274
38	1269	96.5	838	1	PCT-US01-04098A-3151
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42	1176	89.4	824	31	US-10-189-940-128
43	1176	89.4	824	34	US-10-428-275-248
44	1176	89.4	824	39	US-10-971-479-128
45	1174	89.3	820	34	US-10-428-275-272

Sequence 254, App
Sequence 126, App
Sequence 244, App
Sequence 126, App
Sequence 276, App
Sequence 274, App
Sequence 3151, Ap
Sequence 3151, Ap
Sequence 3151, Ap
Sequence 3151, Ap
Sequence 128, App
Sequence 248, App
Sequence 128, App
Sequence 272, App

1021e)

RESULT 3

AAB19727

ID AAB19727 standard; protein; 842 AA.

XX

AC AAB19727;

XX

DT 19-FEB-2001 (first entry)

XX

DE Human SECX Clone 4324229-2 encoded protein.

XX

KW SECX; human; diagnosis; therapy; surface adhesion protein; antitumour;

KW neurological disorder; developmental disorder.

XX

OS Homo sapiens.

XX

PN WO200061754-A2. -102(a)

XX

PD 19-OCT-2000.

XX

PF 07-APR-2000; 2000WO-US009392.

XX

PR 09-APR-1999; 99US-0128514P.

PR 03-MAR-2000; 2000US-0186592P.

PR 06-APR-2000; 2000US-00544511. -102(e)

XX

PA (CURA-) CURAGEN CORP.

XX

PI Fernandez E, Vernet C, Shimkets R;

XX

DR WPI; 2000-679487/66.

DR N-PSDB; AAA88796.

XX

PT SECX polypeptides and the nucleic acids that encode them, useful for

PT diagnosing, preventing and treating e.g. cancers, inflammation, arthritis

PT and immunological disorders.

XX

PS Claim 1; Fig 8; 143pp; English.

XX

CC The present sequence is that of surface adhesion protein-like variant

CC encoded by SECX Clone 4324229-2 (see AAA88796). High expression was

CC detected in the lung. The invention provides novel SECX polynucleotides

CC (see AAA88789-804) and the secreted or membrane-associated proteins

CC encoded by them (see AAB19720-34). SECX polynucleotides, polypeptides and

CC antibodies can be used in the detection, diagnosis and treatment

CC (including gene therapy) of a broad range of pathological states.

CC Therapeutic indications for targeting 4324299 include selected lung,

CC breast and ovarian carcinomas. 4324299 has similarity to human limbic

CC system associated membrane protein (LAMP) and may therefore be important

CC in nerve growth and differentiation, epilepsy, Alzheimer's disease and

CC schizophrenia. It also shows similarity to portions of human Down

CC syndrome-cell adhesion molecule (DS-CAM2), and may therefore be useful in

CC the detection, diagnosis and therapy of developmental and neurological

CC abnormalities such as Down syndrome, mental retardation,

CC holoprosencephaly, agenesis of the corpus callosum and schizencephaly

XX

SQ Sequence 842 AA;

Query Match 98.3%; Score 1292; DB 3; Length 842;

Best Local Similarity 99.6%; Pred. No. 1.3e-112;

Matches 242; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	LLASCGKKFCSRGSRCVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCKLHRAACL	120
Db	61	LLASCGKKFCSRGSRCVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCKLHRAACL	120
Qy	121	LGKRITVIHSKDCFLKGDTCMAGYARLKNVLLALQTRLQPLQEGDSRQDPASQKRLLE	180
Db	121	LGKRITVIHSKDCFLKGDTCMAGYARLKNVLLALQTRLQPLQEGDSRQDPASQKRLLE	180
Qy	181	SLFRDLADGNGHLSSELAQHVLKKQDLDEDLLGCSPGDLLRFDDYNSDSSLTLREFYM	240
Db	181	SLFRDLADGNGHLSSELAQHVLKKQDLDEDLLGCSPGDLLRFDDYNSDSSLTLREFYM	240
Qy	241	AFR	243
		:	
Db	241	AFQ	243